SEQUENCE LISTING

<110> BASCH, Ross S.
ZHANG, Xin-Min

<120> PROTEIN THAT MODULATES THE STABILITY OF TRANSCRIPTIONAL REGULATORY CO MPLEXES REGULATING NUCLEAR HORMONE RECEPTOR ACTIVITY, DNA ENCODING SAME, AND ANTIBODIES THERETO

<130> BASCH=1A

<140> NOT YET ASSIGNED
<141> 2001-11-15

<150> 60/248,191
<151> 2000-11-15

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<170> PatentIn version 3.1

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Met Ser Ile Ser Ser
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Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser
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Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile

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ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat      415
Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser Leu Ser Leu Ile Asp
70                  75                  80                  85

gcc gta atg cct gat gta gta caa aca aga caa caa gct tat aga gat      463
Ala Val Met Pro Asp Val Val Gln Thr Arg Gln Gln Ala Tyr Arg Asp
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Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
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gcc agc caa caa gga tct gca aaa aat gga gaa aac aca gca aat ggg      559
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Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn His Thr Asp Met Met
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Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn Lys Ala Val Val Leu
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cgg ggc cat gaa tct gaa gtt ttt atc tgt gcc tgg aac cct gtt agt      703
Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala Trp Asn Pro Val Ser
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gat ctc cta gca tca ggg tct gga gac tca aca gca aga ata tgg aat      751
Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr Ala Arg Ile Trp Asn
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Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser Asn Lys Asp Val Thr
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gat ggg ttt gcc aga ata tgg act aaa gat ggt aac ctt gct agc acc      943
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Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu Lys Trp Asn Lys Lys
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agt aca gat atg tgc att cat gtc tgt aaa tta gga caa gac aga cct      1183
Ser Thr Asp Met Cys Ile His Val Cys Lys Leu Gly Gln Asp Arg Pro
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Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp
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gac cca act ggc aat ctc ttg gcc tcc tgt tct gac gac atg act tta      1279
Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu
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aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa      1327
Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln
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cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg      1375
His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly
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act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat      1423
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Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr
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ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat      1519
Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp
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ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg      1567
Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp
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aac acg cag aca ggt gct cta gtt cac agc tat agg gga aca ggt gga      1615
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Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp Lys Val Gly Ala Ser
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Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
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Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
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Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
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Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala
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Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
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His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
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Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala
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Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr
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Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln
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Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys
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Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe
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Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu
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Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val
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Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser
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Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val
    370                 375                 380

His Asp Leu Gln Gln His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser
385                 390                 395                 400

Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala
                405                 410                 415

Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly
            420                 425                 430

Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val
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Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys
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tatcctgtgt tgtgacctca tggtttaagt gggaataaag atg agt ata agc agt 175
Met Ser Ile Ser Ser
1 5

gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt 223
Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe
10 15 20

tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc 271
Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser
25 30 35

aat ata aat ggt gcc ctc gtc cca ccc gct gca ttg att tct atc atc 319
Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile
40 45 50

cag aaa ggt cta cag tat gta gaa gca gaa gtt agt att aat gag gat 367
Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val Ser Ile Asn Glu Asp
55 60 65

ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat 415
Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser Leu Ser Leu Ile Asp
70 75 80 85

gcc gta atg cct gat gta gta caa aca aga caa caa gct tat aga gat 463
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90 95 100

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gcc agc caa caa gga tct gca aaa aat gga gaa aac aca gca aat ggg      559
Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu Asn Thr Ala Asn Gly
        120                 125                 130

gag gag aat gga gca cat act ata gca aat aat cat act gat atg atg      607
Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn His Thr Asp Met Met
    135                 140                 145

gaa gtg gat ggg gat gtt gaa atc cct cct aat aaa gct gtt gtg ttg      655
Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn Lys Ala Val Val Leu
150                 155                 160                 165

cgg ggc cat gaa tct gaa gtt ttt atc tgt gcc tgg aac cct gtt agt      703
Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala Trp Asn Pro Val Ser
                170                 175                 180

gat ctc cta gca tca ggg tct gga gac tca aca gca aga ata tgg aat      751
Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr Ala Arg Ile Trp Asn
            185                 190                 195

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Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln Leu Val Leu Arg His
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Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser Asn Lys Asp Val Thr
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tct cta gat tgg aat agt gaa ggt aca ctt cta gca act ggt tcc tat      895
Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu Ala Thr Gly Ser Tyr
230                 235                 240                 245

gat ggg ttt gcc aga ata tgg act aaa gat ggt aac ctt gct agc acc      943
Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly Asn Leu Ala Ser Thr
                250                 255                 260

tta ggg cag cat aaa ggc cct ata ttt gca tta aaa tgg aat aag aaa      991
Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu Lys Trp Asn Lys Lys
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gga aat ttc atc cta agt gct gga gta gac aag act aca att att tgg     1039
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Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe Pro Phe His Ser Ala
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Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn Thr Phe Ala Ser Cys
310                 315                 320                 325

agt aca gat atg tgc att cat gtc tgt aaa tta gga caa gac aga cct     1183
Ser Thr Asp Met Cys Ile His Val Cys Lys Leu Gly Gln Asp Arg Pro
                330                 335                 340

att aaa aca ttc caa gga cat acg aat gaa gta aat gct atc aaa tgg     1231
Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp
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aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa     1327
Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln
    375                 380                 385

cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg     1375
His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly
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act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat     1423
Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp
                410                 415                 420

tct act gtt agg tta tgg gat gta gac cga ggg ata tgc atc cat acc     1471
Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr
            425                 430                 435

ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat     1519
Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp
        440                 445                 450

ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg     1567
Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp
    455                 460                 465

aac acg cag gta tgt ctt cat tat tta aat ggt caa gtg ctc tta aat     1615
Asn Thr Gln Val Cys Leu His Tyr Leu Asn Gly Gln Val Leu Leu Asn
470                 475                 480                 485

tta ggt aga agc att tgc cta tac act ctg cct cac cat ttg gtt gtc     1663
Leu Gly Arg Ser Ile Cys Leu Tyr Thr Leu Pro His His Leu Val Val
                490                 495                 500

att cct ctt gtg gca tta att gaa tta ttg gtt tta aaa taa             1705
Ile Pro Leu Val Ala Leu Ile Glu Leu Leu Val Leu Lys
            505                 510

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His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
        35                  40                  45

Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
    50                  55                  60

Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
65                  70                  75                  80

Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
                85                  90                  95

Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala
            100                 105                 110

Ala Ala Ala Ala Ala Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu
        115                 120                 125

Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
    130                 135                 140

His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
145                 150                 155                 160

Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala
                165                 170                 175

Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr
            180                 185                 190

Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln
        195                 200                 205

Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser
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Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu
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Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly
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Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys
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Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe
    290                 295                 300

Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn
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Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu
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Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val
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Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser
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Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val
    370                 375                 380

His Asp Leu Gln Gln His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser
385                 390                 395                 400

Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala
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Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly
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Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val
        435                 440                 445

Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys
    450                 455                 460

Cys Val His Ile Trp Asn Thr Gln Val Cys Leu His Tyr Leu Asn Gly
465                 470                 475                 480

Gln Val Leu Leu Asn Leu Gly Arg Ser Ile Cys Leu Tyr Thr Leu Pro
                485                 490                 495

His His Leu Val Val Ile Pro Leu Val Ala Leu Ile Glu Leu Leu Val
            500                 505                 510
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Leu Lys

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<210> 6
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<220>
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tcttactaga tgcagtgacc 20

<210> 7
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<220>
<223> Synthetic

<400> 7
gatgagtata agcagtgatg t 21

<210> 8
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<220>
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ctatttttgt tctttccgaa ggtctaata 29

<210> 9
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<220>
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<400> 9
caacagagct tcactttacc c 21

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<220>
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<400> 10
ctagggatgg tttccatga 19

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ggtgatgaac aacaatgtgg aagtcttcag taacttgtga ttggtggttg gctatccagt 120

tgttcatcct cacatcaatg cactgccaat gggttatgtc ctgtgttgtg acctcatggt 180

ttaagtggga ataaag atg agt ata agc agt gat gag gtc aac ttc ttg gta 232
Met Ser Ile Ser Ser Asp Glu Val Asn Phe Leu Val
1 5 10

tat agg tac ttg caa gag tca gga ttt tct cat tct gcg ttt acc ttt 280
Tyr Arg Tyr Leu Gln Glu Ser Gly Phe Ser His Ser Ala Phe Thr Phe
15 20 25

ggt ata gag agc cat ata agt cag tcc aac ata aat ggt gcc ctg gtt 328
Gly Ile Glu Ser His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val
30 35 40

cca ccc gct gca ctc atc tct atc atc cag aaa ggc ctg cag tat gta 376
Pro Pro Ala Ala Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val
45 50 55 60

gag gca gaa gtt agc ata aat gag gat ggc acc tta ttt gat ggt cga 424
Glu Ala Glu Val Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg
65 70 75

ccc atc gag tct ctg tcc ctg ata gat gct gtt atg ccc gat gta gtc 472
Pro Ile Glu Ser Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val
80 85 90

caa aca aga caa caa gcc tac aga gac aag ctt gca cag cag cat gca 520
Gln Thr Arg Gln Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln His Ala
95 100 105

gcc gca gcc gct gcc gct gct gcc gcc act aac cag caa gga tct gca 568
Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gln Gln Gly Ser Ala
110 115 120

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aaa aat gga gag aat aca gca aat ggg gag gag aat gga gca cat acc      616
Lys Asn Gly Glu Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr
125                 130                 135                 140

atc gca aat aat cac act gac atg atg gaa gta gat ggg gat gtg gaa      664
Ile Ala Asn Asn His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu
                145                 150                 155

atc cct tcc aat aaa gcg gtt gtg ctt cgg ggc cat gaa tct gaa gtt      712
Ile Pro Ser Asn Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val
            160                 165                 170

ttc atc tgt gcc tgg aac cct gtt agt gat ctc ctg gta tca ggg tct      760
Phe Ile Cys Ala Trp Asn Pro Val Ser Asp Leu Leu Val Ser Gly Ser
        175                 180                 185

gga gac tcc acg gca aga atc tgg aac ctc agt gag aac agc acg agt      808
Gly Asp Ser Thr Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser
    190                 195                 200

ggc cct acg cag ctc gtg ctt aga cac tgc ata cgg gaa gga ggg cag      856
Gly Pro Thr Gln Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln
205                 210                 215                 220

gac gtg ccc agt aac aag gat gtc acg tct cta gat tgg aat agt gaa      904
Asp Val Pro Ser Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu
                225                 230                 235

ggt aca ctt cta gca act ggg tca tat gat gga ttt gcc aga ata tgg      952
Gly Thr Leu Leu Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp
            240                 245                 250

act aaa gat ggt aat ctt gcc agc acc ttg ggg cag cat aaa ggt cct     1000
Thr Lys Asp Gly Asn Leu Ala Ser Thr Leu Gly Gln His Lys Gly Pro
        255                 260                 265

ata ttt gca tta aag tgg aat aag aaa gga aat ttc atc cta agt gct     1048
Ile Phe Ala Leu Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala
    270                 275                 280

ggc gta gat aag acc acc atc att tgg gat gcg cat act ggt gaa gcc     1096
Gly Val Asp Lys Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala
285                 290                 295                 300

aag cag cag ttt cct ttc cat tca gcc cca gca ttg gat gtt gac tgg     1144
Lys Gln Gln Phe Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp
                305                 310                 315

cag agc aac aac acc ttt gca tct tgt agt aca gat atg tgc att cac     1192
Gln Ser Asn Asn Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His
            320                 325                 330

gtc tgc aaa tta gga caa gac aga cct atc aaa aca ttc cag gga cac     1240
Val Cys Lys Leu Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His
        335                 340                 345

acg aat gaa gta aat gct atc aaa tgg gac cca act ggc aat ctc cta     1288
Thr Asn Glu Val Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu
    350                 355                 360

gcc tcc tgt tca gat gac atg aca ttg aag atc tgg agt atg aag caa     1336
Ala Ser Cys Ser Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln
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365                 370                 375                 380

gat aac tgt gtc cat gat ttg caa gca cat aat aaa gaa att tat act     1384
Asp Asn Cys Val His Asp Leu Gln Ala His Asn Lys Glu Ile Tyr Thr
                385                 390                 395

att aag tgg agt cca aca gga cca ggg aca aat aat cca aat gcc aac     1432
Ile Lys Trp Ser Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn
            400                 405                 410

ctt atg cta gca agt gca tcc ttt gat tct aca gtt agg tta tgg gac     1480
Leu Met Leu Ala Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp
        415                 420                 425

gta gac aga ggg att tgc atc cat act ttg aca aaa cat caa gag ccc     1528
Val Asp Arg Gly Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro
    430                 435                 440

gtg tac agt gtg gct ttt agt cct gat ggc agg tat ctg gca agt ggt     1576
Val Tyr Ser Val Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly
445                 450                 455                 460

tct ttt gac aag tgt gtg cac atc tgg aac aca cag aca ggt gct cta     1624
Ser Phe Asp Lys Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu
                465                 470                 475

gtt cac agt tac agg gga aca ggt gga att ttt gaa gtt tgc tgg aac     1672
Val His Ser Tyr Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn
            480                 485                 490

gca gca gga gac aaa gtt gga gcc agt gct tcg gac ggt tca gtt tgt     1720
Ala Ala Gly Asp Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys
        495                 500                 505

gtc tta gac ctt cgg aaa tag cgttactagt tggaagccat ggaccgacta       1771
Val Leu Asp Leu Arg Lys
    510

tgaatgtgta catagccaca agactatccc tgacccatat actgctatag tcccacttga  1831

accatggcca gtccactaca gc                                           1853


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<213>  Mus musculus

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1               5                   10                  15

Gln Glu Ser Gly Phe Ser His Ser Ala Phe Thr Phe Gly Ile Glu Ser
            20                  25                  30

His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
        35                  40                  45

Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
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50 55 60

Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
65 70 75 80

Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
85 90 95

Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln His Ala Ala Ala Ala Ala
100 105 110

Ala Ala Ala Ala Ala Thr Asn Gln Gln Gly Ser Ala Lys Asn Gly Glu
115 120 125

Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
130 135 140

His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Ser Asn
145 150 155 160

Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala
165 170 175

Trp Asn Pro Val Ser Asp Leu Leu Val Ser Gly Ser Gly Asp Ser Thr
180 185 190

Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Pro Thr Gln
195 200 205

Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser
210 215 220

Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu
225 230 235 240

Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly
245 250 255

Asn Leu Ala Ser Thr Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu
260 265 270

Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys
275 280 285

Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe
290 295 300

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Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn
305                 310                 315                 320

Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu
                325                 330                 335

Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val
            340                 345                 350

Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser
        355                 360                 365

Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val
    370                 375                 380

His Asp Leu Gln Ala His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser
385                 390                 395                 400

Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala
                405                 410                 415

Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly
            420                 425                 430

Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val
        435                 440                 445

Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys
    450                 455                 460

Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr
465                 470                 475                 480

Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp
                485                 490                 495

Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu
            500                 505                 510

Arg Lys
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<210> 13
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<400> 13

Cys Gly Val Ser His Gln Asn Pro Ser Lys
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caggcttata gagataaact tgca 24

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<400> 16
gtaagactct ccaactccca at 22

<210> 17
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 17

Thr Gln Thr Gly Ala Leu Val His Ser Tyr Arg Gly Thr Gly Gly Ile
1 5 10 15

Phe Glu Val Cys Trp Asn Ala Cys Ala Gly Asp Lys Val Gly Ala Ser
20 25 30

Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu Arg
35 40